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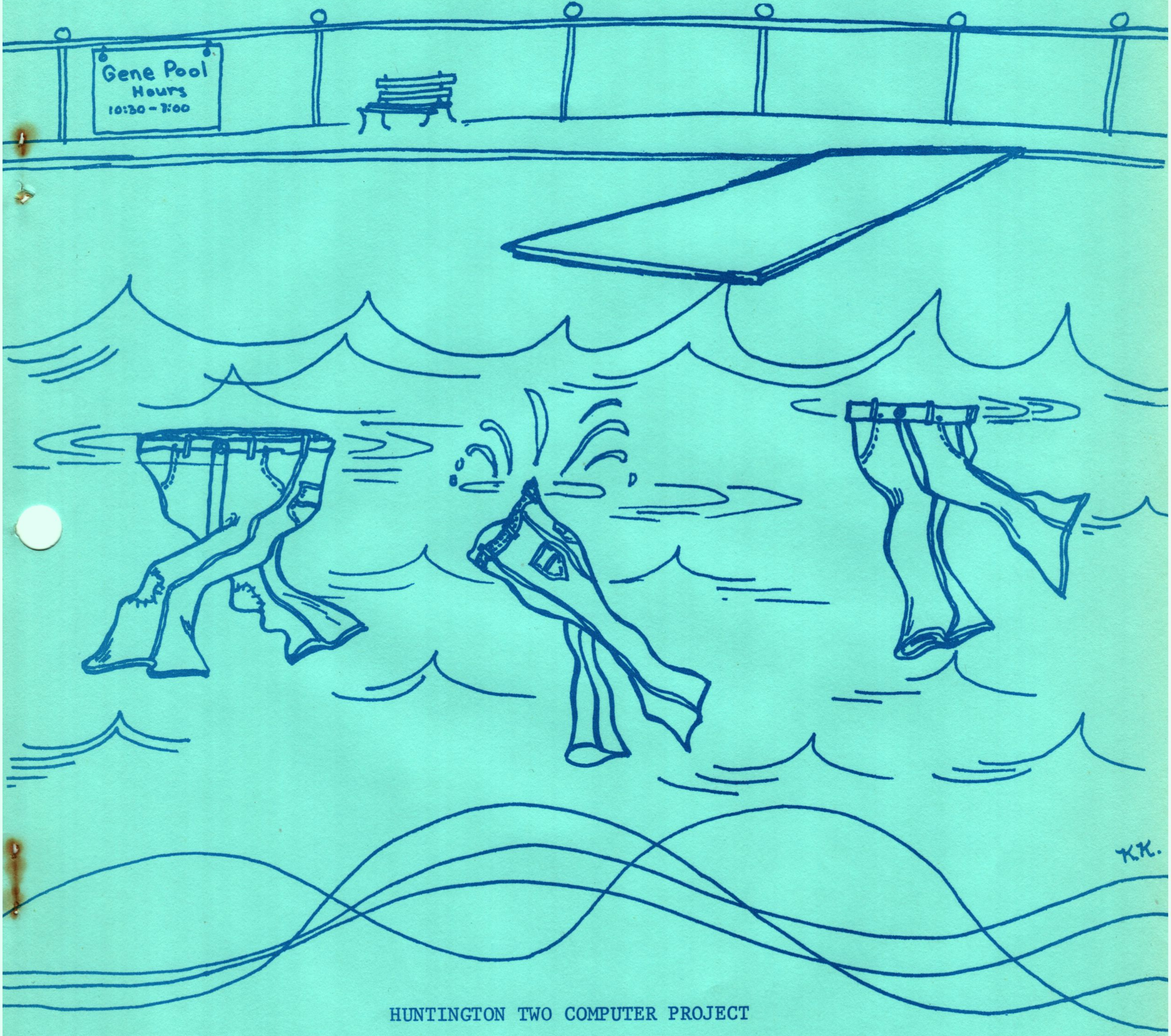
STUDENT MANUAL

THE HARDY-WEINBERG PRINCIPLE

HARDY



HUNTINGTON TWO COMPUTER PROJECT

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8 September 1973

The work of the Huntington Two Computer Project is partially supported by the National Science Foundation, Grant GW-5883.
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HARDY

STUDENT MANUAL

With the *HARDY* program you'll be venturing into the field of population genetics: the study of the mechanism of gene inheritance as seen in its effects on a population. We will define a population to be the total number of organisms of a single species found within a defined area.

The *HARDY* program will involve you in studying certain single-gene, non-linked characteristics within a population of your choosing. For some of these traits, a large majority of the population will show dominance; for the remaining traits, a majority of the population will exhibit the recessive trait. What do the terms *dominant* and *recessive* imply about the relative frequencies of the dominant and recessive phenotypes within the population? If a trait is dominant, does that mean it will become more and more widespread throughout the population and that the recessive trait will eventually disappear? Does the genetic make-up of a population tend to remain stable or does it tend to change? And if changes occur, what factors are responsible?

The answers to many of these questions will be found in a biological principle first formulated in 1908 by G. H. Hardy, an English mathematician, and W. Weinberg, a German physician. The Hardy-Weinberg Principle states that the genotypic ratios for a single-gene characteristic remain constant within a population from one generation to the next, provided certain conditions are met. The Hardy-Weinberg Principle is especially valuable because, in its mathematical form, it gives us a simple way of determining genotypic ratios for a population with regard to a specific trait, once the proportion of recessives within the population is known.

To obtain real-life data on the genetic make-up of a population with respect to certain characteristics, you can carry out surveys to determine the proportion of recessives within the population for each characteristic. You can then use the *HARDY* program to analyze your data, to give you the genotypic ratios for each characteristic.

Because you will be carrying out surveys on populations to obtain data for analysis, you will have to learn a little about sound sampling techniques. Also, in order to understand the mathematical formulation of the Hardy-Weinberg Principle, you'll have to learn a little (but only a little) about probability along the way. The heart of the program is, of course, the Hardy-Weinberg Principle -- its formulation, its meaning and significance, its application. We hope that *HARDY* will give you some idea of what population genetics is all about.

INSTRUCTION FOR RUNNING *HARDY*

The first time you use *HARDY*, you will receive a brief explanation of the Hardy-Weinberg Principle and a population of rats to work with. For all subsequent runs, you can either use your own data or work with a rat population generated by the computer.

If you have compiled your own data from a sample population and want it analyzed for the proportion and number of the population that is homozygous dominant, heterozygous dominant, and homozygous recessive with regard to the trait in question, you will have to input the total number of organisms examined and the number showing the recessive trait.

The computer will first calculate the proportion of organisms showing the recessive trait $\left(\frac{\text{number showing recessive trait}}{\text{total number of organisms examined}}\right)$; this proportion will be designated Q^2 in the program. The next calculation will be for the frequency of the recessive allele within the gene pool of the population -- which, of course, is given by the value of Q. Finally the computer will calculate and print out the genotypic ratios as well as the actual number of organisms of each genotype.

If you do not have data of your own, you can request the computer to sample one of two rat populations generated by the program. The "original" rat population (which you sampled the first time you used the program) has a fixed proportion of recessives; the "new" population has a varying proportion of recessives. For whichever population you choose, you will first have to enter the number or rats you want to sample. The computer will then generate data for the number of rats showing the dominant trait (short hair) and the number showing the recessive trait (long hair). After this, the computer will calculate and print the value of Q^2 and Q, followed by the genotypic ratios for the rat population and the number of rats of each genotype.

The program can be repeated as many times as you wish.

* * *

The *HARDY* program will involve you in the study of a single-gene trait within a population. You may, if you wish, use fruit flies or any other experimental animal for your study, but there is a population at hand which can be sampled easily and which has a significant number of individuals. This is the human population within your community.

There are several traits which can be sampled for easily within a human population. The following are only three of the possibilities:

1) Taster of PTC vs. nontaster

Phenylthiocarbamide tastes bitter to those who are dominant for this characteristic.

2) Free ear lobe vs. attached ear lobe

The ear lobe can hang free from the facial skin or it can be fully attached. The condition where the ear lobe hangs free is dominant.

3) Tongue roller vs. non-tongue roller

The ability to stick the tongue out and curl up the sides is dominant over not being able to do so.

THE SAMPLE POPULATION

You and your classmates are going to select a sample from your community for which to do a survey with regard to these three traits. In sampling a population, there are several things to keep in mind. First, remember that you are only sampling, which means that you will not be surveying the total population; your sample must be large enough, however, to be significant compared to the total population. For example, suppose your community contains 10,000 organisms and you sample 10,000 organisms. The results of your survey will be extremely accurate, but this procedure may be so time-consuming and expensive as to be impractical. If you sample only 50 organisms, however, the number is so few that the results of your survey may not be representative of the population. In deciding upon a sample size, you will have to choose a number that will be significant as well as practical for sampling. In the example above, a sample size of 1000 to 2000 would have been a fair figure.

The second consideration is that your sample must be a random one; in other words, the group of organisms being sampled should be a representative cross-section of the total population. If this is not the case, if the sample is chosen only out of convenience, for example, your results may be completely non-representative of the total population.

SURVEY PROCEDURE

1) Break up into small survey teams (2 or 3 individuals per group). Each group should survey a separate area of the community.

2) Record the results of your survey systematically and accurately. You might find a record sheet like the one below helpful:

MALE	FEMALE	PTC		EAR LOBES		TONGUE	
		TASTER	NONTASTER	FREE	ATTACHED	ROLLER	NONROLLER

3) When your team returns to class after completing the survey, pool your data with the other survey teams by placing totals for each trait sampled on the board.

CALCULATIONS AND RESULTS

Now you can run the *HARDY* program using the pooled data for each trait surveyed, entering the data for one trait at a time. If possible, try to calculate the genotypic ratios for each trait on your own, using the Hardy-Weinberg Principle. You can then run *HARDY* with each of the three sets of data to obtain a check on your calculations.

You may find it helpful to keep records of each set of calculations and the results of each subsequent run. A sample data sheet is included in this section.

The following problems are similar to those presented in the analysis of your survey data. Each of these problems can be solved by applying the Hardy-Weinberg Principle.

PROBLEM 1: Assume that the gene for white wool in sheep is dominant over the gene for black wool. If 250 out of 1000 sheep observed in a large population have black wool, what per cent are homozygous white and what per cent are heterozygous white?

PROBLEM 2: If we know that 128 out of 200 people surveyed for being tasters or nontasters of PTC show the dominant characteristic, what per cent of the general population (approximately 1000 people) are heterozygous?

PROBLEM 3: Polydactilism in humans is the condition of being six-fingered. Although this condition is dominant over the five-fingered condition, 97% of the general population are five-fingered. What per cent of the population are homozygous dominant and what per cent are heterozygous?

SAMPLE DATA SHEET

YOUR COMPUTATION

Trait ____________________

Number Surveyed ____________________

Number Recessives ____________________

Proportion Recessives (Q^2) ____________________

Frequency Recessive Allele (Q) ____________________

Frequency Dominant Allele (P) ____________________

Proportion Homozygous Dominant (P^2) ____________________

Number ____________________

Proportion Heterozygous Dominant (2PQ) ____________________

Number ____________________

PROGRAM COMPUTATION

Trait ____________________

Number Surveyed ____________________

Number Recessives ____________________

Proportion Recessives (Q^2) ____________________

Frequency Recessive Allele (Q) ____________________

Frequency Dominant Allele (P) ____________________

Proportion Homozygous Dominant (P^2) ____________________

Number ____________________

Proportion Heterozygous Dominant (2PQ) ____________________

Number ____________________